



#4

	9	18	27	36	45	54
5' GGC TTC TGG GAG CNA CCG CTC CGC TCG TCT CGT TGG TTC CGG AGG TCG CTG CGG						
	63	72	81	90	99	108
CGG TGG GAA ATG CTG GCG CGC GCG GCG CAC TGG GGC CCT TTT GCT GAG M L A R A A R G H W G P F A E						
	117	126	135	144	153	162
GGG CTC TCT ACT GGC TTC TGG CCG CGC TCC GGC CGC GCC TCC TCT GGA TTG CCC G L S T G F W P R S G R A S S G L P						
	171	180	189	198	207	216
CGA AAC ACC GTG GTA CTG TTC GTG CCG CAG CAG GCC TGG GTG GAG CGA R N T V V L F V P Q Q E A W V E R						
	225	234	243	252	261	270
ATG GGC CGA TTC CAC CCG ATC CTG GAG CCT GGT TTG AAC ATC CTC ATC CCT GTG M G R F H R I L E P G G L N I L I P V						
	279	288	297	306	315	324
TTA GAC CGG ATC CGA TAT GTG CAG AGT CTC AAG GAA ATT GTC ATC AAC GTG CCT L D R I R Y V Q S L K E E I V I N V P						
	333	342	351	360	369	378
GAG CAG TCG GCT GTG ACT CTC GAC AAT GTA ACT CTG CAA ATC GAT GGA GTC CTT E Q S A V T L L D N V T L L Q I D G V L						

FIGURE 1A

387	396	405	414	423	432
TAC CTG CGC ATC ATG GAC CCT TAC AAG GCA AGC TAC GGT GTG GAC GAC CCT GAG					
Y L R I M D P Y K A S Y G V E D P E					
441	450	459	468	477	486
TAT GCC GTC ACC CAG CTA GCT CAA ACA ACC ATG AGA TCA GAG CTC GGC AAA CTC					
Y A V T Q L A Q T T M R S E L G K L					
495	504	513	522	531	540
TCT NTG GAC AAA GTC TTC CGG GAA CGG GAG TCC CTG AAT GCC AGC ATT GTG GAT					
S X D K V F R E R E S L N A S I V D					
549	558	567	576	585	594
GCC ATC AAC CAA GCT GCT GAC TGC TGG GGT ATC CGC TGC CTN CGT TAT GAG ATC					
A I N Q A A A D C W G I R C L R Y E I					
603	612	621	630	639	648
AAG GAT ATC CAT GTG CCA CCC CGG GTG AAA GAG TCT ATG CAG ATG CAG GTG GAG					
K D I H V P P R V K E S M Q V E					
657	666	675	684	693	702
GCA GAG CGG CGG AAA CGG GCC ACA GTT CTA GAG TCT TCT GAG GGG ACC CGA GAG TCG					
A E R R R K R A T V L E S E G T R E S					
711	720	729	738	747	756
GCC ATC AAT GTG GCA GAA GGG AAG AAA CAG GCC CAG ATC CTG GCC TCC GAA GCA					
A I N V A E G K Q A Q I L A S E A					

FIGURE 1B

765	774	783	792	801	810
GAA AAG GCT GAA CAG ATA AAT CAG GCA GGA GAG GCC AGT GCA GTT CTG GCG					
E K A E Q I N Q A A G E A S A V L A					
819	828	837	846	855	864
AAG GCC AAG GCT AAA GCT GAA GCT ATT CGA ATC CTG GCT GCA GCT CTG ACA CAA					
K A K A A K A E A I R I L A A A L T Q					
873	882	891	900	909	918
CAT AAT GGA GAT GCA GCA GCT TCA CTG ACT GTG GCC GAG CAG TAT GTC AGC GCG					
H N G D A A A A S L T V A E Q Y V S A					
927	936	945	954	963	972
TTC TCC AAA CTG GCC AAG GAC TCC AAC ACT ATC CTA CTG CCC TCC AAC CCT GGC					
F S K L A K A K D S N T I L L P S N P G					
981	990	999	1008	1017	1026
GAT GTC ACC AGC ATG GTG GCT GCT CAG GCC ATG GGT GTA TAT GGA GCC CTC ACC AAA					
D V T S M V A Q A M G V Y G A L T K					
1035	1044	1053	1062	1071	1080
GCC CCA GTG CCA GGG ACT CCA GAC TCA CTC TCC AGT GGG AGC AGC AGA GAT GTC					
A P V P G T P D S L S S G S S R D V					
1089	1098	1107	1116	1125	1134
CAG GGT ACA GAT GCA AGT NTT GAT GAG GAA CTT GAT CGA GTC AAG ATG AGT TAG					
Q G T D A S X D E E L D R V K M S *					

FIGURE 1C

4001 343660

1143 TGG AGC TGG GCT TNG CCA GGG AGT CTG GGG ACA AGG AAG CAG ATT TTC CTG ATT 1188

1152

1161

1170

1179

1188

3'

FIGURE 1D

FIGURE 2A

FIGURE 2B

FIGURE 2C

Library	Lib Description	Abun	Pct Abun
PROSTUT03	prostate tumor, 67 M, match to PROSNOT05	2	0.0703
COLNNOT05	colon, 40 M, match to COLNCRT01	2	0.0577
TESTNOT03	testis, 37 M	1	0.0557
LIVRNOT02	liver, 32 F	1	0.0515
HUVENOB01	HUVEC endothelial cell line, control	1	0.0418
LVENNOT03	heart, left ventricle, 31 M	1	0.0336
PROSTUT01	prostate tumor, 50 M, match to PROSNOT02	1	0.0309
PANCTUT02	pancreatic tumor, carcinoma, 45 F	1	0.0288
KERANOT01	keratinocytes, neonatal M	1	0.0227
CRBLNOT01	brain, cerebellum, 69 M	1	0.0194
LUNGNOT04	lung, 2 M	1	0.0182
PGANNT01	paraganglia, 46 M	1	0.0159
BRSTTUT01	breast tumor, 55 F, match to BRSTNOT02	1	0.0150

FIGURE 3